AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

LISTING OF CLAIMS:

1. (original): A method for examining a gene comprising detecting a variation in nucleic-acid bases in at least two or more positions within a gene region containing a glaucoma-related gene coding region and/or an upstream region and predicting any future development of glaucoma using said variation as an index.

2. (original): The method according to Claim 1 wherein the glaucoma-related gene is a myocilin (MYOC) gene.

3. (currently amended): The method according to Claim 1 ~~or 2~~ wherein the gene region is the nucleic-acid base sequence represented by SEQ ID No: 1.

4. (currently amended): The method according to Claim 1 ~~any one of Claims 1 to 3~~ wherein the variation in a base is a substitution, deletion and/or insertion.

5. (original): The method according to Claim 3 which detects any of the group consisting of, in the nucleic-acid base sequence represented by SEQ ID No: 1, the C-to-A substitution at position 194; the A-to-C substitution at position 199; the G-to-A substitution at position 324; the C-to-T substitution at position 1051; the C-to-T substitution at position 1084; the T-to-C substitution at position 1627; the T-to-C substitution at position 1685; the C-to-T substitution at position 1756;

the G-to-C substitution at position 1853; the G-to-A substitution at position 2830; the A-to-G substitution at position 3371; the G-to-A substitution at position 4037; and the G-to-A substitution at position 4346.

6. (original): The method according to Claim 3 which detects at least two or more simultaneous substitutions selected from the group consisting of, in the nucleic-acid base sequence represented by SEQ ID No: 1, the C-to-A substitution at position 194; the C-to-T substitution at position 1084; the T-to-C substitution at position 1627; the G-to-A substitution at position 4037; and the G-to-A substitution at position 4346.

7. (original): The method according to Claim 3 which detects at least two or more simultaneous substitutions selected from the group consisting of, in the nucleic-acid base sequence represented by SEQ ID No: 1, the C-to-T substitution at position 1051; the T-to-C substitution at position 1685; the C-to-T substitution at position 1756; and the G-to-C substitution at position 1853.

8. (original): A method for examining a gene comprising detecting at least one substitution of the group consisting of, in the nucleic-acid base sequence represented by SEQ ID No: 1, the A-to-C substitution at position 199; the G-to-A substitution at position 324; the C-to-T substitution at position 1051; the C-to-T substitution at position 1084; the T-to-C substitution at position 1627; the T-to-C substitution at position 1685; the C-to-T substitution at position 1756; the G-to-C substitution at position 1853; the G-to-A substitution at position 2830; and the A-to-G substitution at position 3371 and predicting any future development of glaucoma using said variation as an index.

9. (currently amended): The method according to Claim 1~~any one of Claims 1 to 8~~ wherein the glaucoma is primary open-angle glaucoma and/or normal tension glaucoma.

10. (currently amended): The method according to Claim 1~~any one of Claims 1 to 9~~ wherein the variation is detected using an oligonucleotide capable of specifically forming a hybrid with a part of a gene region containing a glaucoma-related gene coding region and/or an upstream region.

11. (original): A primer function-possessing oligonucleotide wherein the oligonucleotide, which is capable of specifically forming a hybrid with a part of a gene region containing a glaucoma-related gene coding region and/or an upstream region, is at least one or more selected from the group consisting of:

1) an oligonucleotide consisting of a nucleic-acid base sequence represented by any of SEQ ID Nos. 2 to 27;

2) a strand complementary with the oligonucleotide according to the above-mentioned 1);

3) an oligonucleotide capable of hybridizing under a stringent condition with the oligonucleotide according to the above-mentioned 1) or 2);

4) an oligonucleotide having a homology of about 60% with the oligonucleotide according to any one of the above-mentioned 1) to 3);

5) an oligonucleotide having a nucleic-acid base sequence whose 1 or more base of oligonucleotides according to the above-mentioned 1) to 4)was subjected to a variation such as a substitution, deletion, insertion or addition.

12. (currently amended): The method according to Claim 1~~any one of Claims 1 to 9~~ comprising performing a nucleic acid amplification process using at least one oligonucleotide selected from the oligonucleotides according to Claim 11.

13. (currently amended): An examination reagent or examination reagent kit comprising a reagent employed in the examination method according to Claim 12~~any one of Claims 1 to 10 or Claim 12.~~

14. (new): The method according to Claim 2 wherein the gene region is the nucleic-acid base sequence represented by SEQ ID No: 1.

15. (new): The method according to Claim 2 wherein the variation in a base is a substitution, deletion and/or insertion.

16. (new): The method according to Claim 3 wherein the variation in a base is a substitution, deletion and/or insertion.

17. (new): The method according to Claim 2 wherein the glaucoma is primary open-angle glaucoma and/or normal tension glaucoma.

18. (new): The method according to Claim 2 wherein the variation is detected using an oligonucleotide capable of specifically forming a hybrid with a part of a gene region containing a glaucoma-related gene coding region and/or an upstream region.

19. (new): The method according to Claim 3 wherein the glaucoma is primary open-angle glaucoma and/or normal tension glaucoma.

20. (new): The method according to Claim 3 wherein the variation is detected using an oligonucleotide capable of specifically forming a hybrid with a part of a gene region containing a glaucoma-related gene coding region and/or an upstream region.